

	Ref #	Hits	Search Text
1	S1	1	("7208576").PN.
2	S2	0	C c r g d v l d
3	S3	0	cys cys arg gly asp val leu asp
4	S4	9	"9514714"
5	S5	8	"9111458"
6	S6	5	"9859040"
7	S7	3	dudich-elena-ivanovna.in.
8	S8	2	semenkova-lidia-nikolaevna.in.
9	S9	0	semenkova-lidia.in.
10	S10	2	dudich-igor-vyacheslavovitch.in.
11	S11	1	tatulov-edward-borisovitch.in.
12	S12	1	zubov-dimitry-lvovicth.in.
13	S13	14	korpela-timo-kalevi.in.
14	S14	0	apocyclin-1
15	S15	1	apocyclin-a
16	S16	0	".alpha.fetoprotein"
17	S17	9912	fetoprotein
18	S18	12826	S17 or AFP
19	S19	93	S18 same apoptosis
20	S20	5	S19 and (Arg adj Gly adj Asp)
21	S21	46	S19 and (cyclic or bridge)
22	S22	6	S19 same (cyclic or bridge)

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OM protein - protein search, using sw model

Run on: August 21, 2007, 20:41:45 ; Search time 188 Seconds
(without alignments)
23.426 Million cell updates/sec

Title: US-10-530-779-1
Perfect score: 58
Sequence: 1 CCRGDVLDC 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_200701:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*
11: geneseqp2007s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Match	Length	DB	ID	Description	
1	58	100.0	9	8	ADM96257	Adm96257 Human alp	
2	58	100.0	60	8	ADM96252	Adm96252 Human alp	
3	58	100.0	192	9	ADW97076	Adw97076 Human alp	
4	58	100.0	192	9	ADW97081	Adw97081 Human non	
5	58	100.0	390	9	ADW97078	Adw97078 Human alp	
6	58	100.0	390	9	ADW97082	Adw97082 Human non	

7	58	100.0	393	9	ADW97083	Adw97083	Human non
8	58	100.0	393	9	ADW97079	Adw97079	Human alp
9	58	100.0	448	8	ABM83883	Abm83883	Human dia
10	58	100.0	448	9	AED96373	Aed96373	Human C-r
11	58	100.0	551	9	AED96372	Aed96372	Human C-r
12	58	100.0	555	8	ABM85000	Abm85000	Human dia
13	58	100.0	573	8	ABM84999	Abm84999	Human dia
14	58	100.0	590	2	AAW01023	Aaw01023	Alpha-foe
15	58	100.0	590	10	AEF64991	Aef64991	Recombina
16	58	100.0	591	9	ADW97070	Adw97070	Human mat
17	58	100.0	591	9	ADW97074	Adw97074	Human non
18	58	100.0	591	9	ADW97094	Adw97094	Non-glyco
19	58	100.0	591	9	ADY62718	Ady62718	Human alp
20	58	100.0	591	9	ADY62716	Ady62716	Human alp
21	58	100.0	592	9	AED96371	Aed96371	Human C-r
22	58	100.0	597	10	AEF65000	Aef65000	Recombina
23	58	100.0	609	4	AAU07130	Aau07130	Human Alp
24	58	100.0	609	6	ABU56593	Abu56593	Lung canc
25	58	100.0	609	7	ADD84895	Add84895	Human alp
26	58	100.0	609	7	ADD84896	Add84896	Human alp
27	58	100.0	609	8	ADL12727	Adl12727	Human ste
28	58	100.0	609	8	ADQ29647	Adq29647	Human col
29	58	100.0	609	8	ABM80568	Abm80568	Tumour-as
30	58	100.0	609	9	ADW97068	Adw97068	Human pre
31	58	100.0	609	9	ADW97093	Adw97093	Human non
32	58	100.0	609	9	ADW97072	Adw97072	Human non
33	58	100.0	609	9	ADY62714	Ady62714	Human alp
34	58	100.0	609	9	AED96370	Aed96370	Human C-r
35	58	100.0	609	10	AEF05902	Aef05902	Human alp
36	58	100.0	609	10	AEF05903	Aef05903	Human alp
37	58	100.0	609	10	AEF69959	Aef69959	Colorecta
38	58	100.0	609	10	AEH64969	Aeh64969	Human (al
39	58	100.0	631	4	AAU31987	Aau31987	Novel hum
40	58	100.0	675	10	AEF64998	Aef64998	Recombina
41	52	89.7	192	2	AAR99224	Aar99224	Recombina
42	52	89.7	192	4	AAB62069	Aab62069	Mature rH
43	52	89.7	389	2	AAR99222	Aar99222	Recombina
44	52	89.7	389	4	AAB62071	Aab62071	Mature rH
45	52	89.7	393	2	AAR99223	Aar99223	Recombina

ALIGNMENTS

RESULT 1

ADM96257

ID ADM96257 standard; peptide; 9 AA.

XX

AC ADM96257;

XX

DT 15-JUL-2004 (first entry)

XX

DE Human alpha-fetoprotein peptide #9 related to apoptosis modulation.

XX

KW apoptotic cell death; apoptotically active site; human alpha-fetoprotein;

KW human serum albumin; immunosuppressive; virucide;

KW apoptosis signaling modulator; apoptotic regulatory pathway;

OM protein - protein search, using sw model

Run on: August 21, 2007, 20:42:57 ; Search time 345 Seconds
 (without alignments)
 27.968 Million cell updates/sec

Title: US-10-530-779-1
 Perfect score: 58
 Sequence: 1 CCRGDVLDC 9

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : UniProt_8.4:*
 1: uniprot_sprot:*
 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	58	100.0	609	1 FETA_GORGO	P28050 gorilla gor
2	58	100.0	609	1 FETA_HUMAN	P02771 homo sapien
3	58	100.0	609	1 FETA_PANTR	Q28789 pan troglod
4	51	87.9	615	1 FETA_CHICK	P84407 gallus gall
5	50	86.2	527	2 Q8JIA9_SPHPU	Q8jia9 sphenodon p
6	49	84.5	608	2 Q7TSF3_MARMO	Q7tsf3 marmota mon
7	49	84.5	609	1 FETA_CANFA	Q8mju5 canis famil
8	49	84.5	610	2 Q8MJ76_PIG	Q8mj76 sus scrofa
9	49	84.5	907	2 Q3H1T0_9ACTO	Q3hlt0 nocardioide
10	47	81.0	172	2 Q2ZL72_SHEPU	Q2zl72 shewanella
11	47	81.0	238	2 Q3QB87_9GAMM	Q3qb87 shewanella
12	47	81.0	376	1 PDXB_SHEON	Q8ecr2 shewanella
13	47	81.0	376	2 Q2Z8I9_9GAMM	Q2z8i9 shewanella
14	47	81.0	413	2 Q2WYL7_9GAMM	Q2wyl7 shewanella
15	46	79.3	94	2 Q5G9V3_TUPGB	Q5g9v3 tupaia glis

16	46	79.3	417	2	Q86YG0_HUMAN	Q86yg0 homo sapien
17	46	79.3	476	2	Q3I349_BOSIN	Q3i349 bos indicus
18	46	79.3	576	2	Q8C7C7_MOUSE	Q8c7c7 mus musculu
19	46	79.3	583	2	Q6B3Z0_ELEMA	Q6b3z0 elephas max
20	46	79.3	600	1	ALBU_MACMU	Q28522 macaca mula
21	46	79.3	607	1	ALBU_BOVIN	P02769 bos taurus
22	46	79.3	607	1	ALBU_EQUAS	Q5xle4 equus asinu
23	46	79.3	607	1	ALBU_HORSE	P35747 equus cabal
24	46	79.3	607	1	ALBU_PIG	P08835 sus scrofa
25	46	79.3	607	1	ALBU_SHEEP	P14639 ovis aries
26	46	79.3	607	2	Q3T478_BOMMX	Q3t478 bombina max
27	46	79.3	607	2	Q3T479_BOMMX	Q3t479 bombina max
28	46	79.3	608	1	ALBU_CANFA	P49822 canis famil
29	46	79.3	608	1	ALBU_FELCA	P49064 felis silve
30	46	79.3	608	1	ALBU_MOUSE	P07724 mus musculu
31	46	79.3	608	1	ALBU_RABIT	P49065 oryctolagus
32	46	79.3	608	1	ALBU_RAT	P02770 rattus norv
33	46	79.3	608	2	Q95VB7_SCHMA	Q95vb7 schistosoma
34	46	79.3	608	2	Q5EG49_MICFO	Q5eg49 microtus fo
35	46	79.3	608	2	Q3TV03_MOUSE	Q3tv03 mus musculu
36	46	79.3	608	2	Q5EG48_MICFO	Q5eg48 microtus fo
37	46	79.3	608	2	Q5U3X3_RAT	Q5u3x3 rattus norv
38	46	79.3	608	2	Q6WDN9_CAVPO	Q6wdn9 cavia porce
39	46	79.3	608	2	Q8C7H3_MOUSE	Q8c7h3 mus musculu
40	46	79.3	608	2	Q546G4_MOUSE	Q546g4 mus musculu
41	46	79.3	609	1	ALBU_HUMAN	P02768 homo sapien
42	46	79.3	609	1	ALBU_MERUN	O35090 meriones un
43	46	79.3	609	2	Q56G89_HUMAN	Q56g89 homo sapien
44	46	79.3	609	2	Q645G4_HUMAN	Q645g4 homo sapien
45	46	79.3	609	2	Q5NVH5_PONPY	Q5nvh5 pongo pygma

ALIGNMENTS

RESULT 1

FETA_GORGO

ID FETA_GORGO STANDARD; PRT; 609 AA.
AC P28050;
DT 01-AUG-1992, integrated into UniProtKB/Swiss-Prot.
DT 01-AUG-1992, sequence version 1.
DT 18-APR-2006, entry version 44.
DE Alpha-fetoprotein precursor (Alpha-fetoglobulin) (Alpha-1-fetoprotein).
DE fetoprotein).
GN Name=AFP;
OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Gorilla.
OX NCBI_TaxID=9595;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=91169517; PubMed=1706310;
RA Ryan S.C., Zielinski R., Dugaiczek A.;
RT "Structure of the gorilla alpha-fetoprotein gene and the divergence of
RT primates.";
RL Genomics 9:60-72(1991).

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OM protein - protein search, using sw model

Run on: August 21, 2007, 20:45:01 ; Search time 30 Seconds
(without alignments)
28.865 Million cell updates/sec

Title: US-10-530-779-1
Perfect score: 58
Sequence: 1 CCRGDVLDC 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	58	100.0	609	1	FPGO	alpha-fetoprotein
2	58	100.0	609	1	FPHU	alpha-fetoprotein
3	58	100.0	609	2	JC4258	alpha-fetoprotein
4	46	79.3	265	2	I46986	albumin - dog (fra
5	46	79.3	453	2	A05139	serum albumin - mo
6	46	79.3	600	2	A47391	serum albumin prec
7	46	79.3	605	1	ABPGS	serum albumin prec
8	46	79.3	607	1	ABBOS	serum albumin prec
9	46	79.3	607	1	ABHOS	serum albumin prec
10	46	79.3	607	1	ABSHS	serum albumin prec
11	46	79.3	608	1	ABRTS	serum albumin prec
12	46	79.3	608	2	S57632	serum albumin prec
13	46	79.3	609	1	ABHUS	serum albumin prec

14	46	79.3	609	2	JC5838	albumin - Mongolia
15	44	75.9	382	2	A37253	serum albumin - bu
16	44	75.9	599	1	A54906	afamin precursor -
17	44	75.9	608	2	A53195	afamin precursor -
18	43	74.1	615	1	ABCHS	serum albumin prec
19	42	72.4	608	1	ABXL68	68K serum albumin
20	40	69.0	826	2	T43638	caspase-related pr
21	39	67.2	605	1	FPMS	alpha-fetoprotein
22	39	67.2	608	1	ABONS1	serum albumin 1 pr
23	39	67.2	608	1	ABONS2	serum albumin 2 pr
24	38	65.5	240	2	A46587	extracellular hemo
25	38	65.5	468	2	S02514	nifB protein - Kle
26	38	65.5	485	2	S64945	probable membrane
27	38	65.5	519	2	A54590	GAGA transcription
28	38	65.5	611	1	FPRT	alpha-fetoprotein
29	38	65.5	888	2	H88085	protein T11F1.8 [i
30	37	63.8	138	2	S29299	phospholipase A2 (
31	37	63.8	352	2	T23464	hypothetical prote
32	37	63.8	870	2	G86450	F5D14.31 protein -
33	36	62.1	122	1	PSVII	phospholipase A2 i
34	36	62.1	122	2	A25806	phospholipase A2 (
35	36	62.1	122	2	S62780	phospholipase A2 (
36	36	62.1	138	1	PSVIAA	phospholipase A2 (
37	36	62.1	138	1	PSVIAC	phospholipase A2 (
38	36	62.1	138	2	S59522	phospholipase A2 (
39	36	62.1	138	2	S10333	ammodytoxin B prec
40	36	62.1	138	2	I51386	phospholipase A2 (
41	36	62.1	277	2	S64710	cysteine proteinas
42	36	62.1	277	2	A55315	cysteine proteinas
43	36	62.1	277	2	JC5410	CPP32 protein - mo
44	36	62.1	404	2	E81588	conserved hypothet
45	36	62.1	419	1	WJFFH2	homeotic protein H

ALIGNMENTS

RESULT 1

FPGO

alpha-fetoprotein precursor - gorilla

C;Species: Gorilla gorilla (gorilla)

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C;Accession: A37970

R;Ryan, S.C.; Zielinski, R.; Dugaiczky, A.

Genomics 9, 60-72, 1991

A;Title: Structure of the gorilla alpha-fetoprotein gene and the divergence of primates.

A;Reference number: A37970; MUID:91169517; PMID:1706310

A;Accession: A37970

A;Molecule type: DNA

A;Residues: 1-609 <RYA>

A;Cross-references: UNIPROT:P28050; UNIPARC:UPI000012A6F8; GB:M38272;

NID:g817963; PIDN:AAA73520.1; PID:g177041

C;Genetics:

A;Map position: 4q11-12

A;Introns: 29/1; 46/2; 90/3; 161/2; 205/3; 238/2; 281/3; 353/2; 397/3; 430/2; 476/3; 551/2; 595/3